

#2

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RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/895,072

DATE: 07/23/2001  
TIME: 13:19:44

Input Set : A:\210119US0CONT.txt  
Output Set: N:\CRF3\07232001\I895072.raw

3 <110> APPLICANT: CANFIELD, WILLIAM M  
5 <120> TITLE OF INVENTION: METHODS FOR PRODUCING HIGHLY PHOSPHORYLATED LYSOSOMAL HYDROLASES

7 <130> FILE REFERENCE: 210119US0CONT  
C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/895,072  
C--> 9 <141> CURRENT FILING DATE: 2001-07-02  
9 <150> PRIOR APPLICATION NUMBER: 60/153,831  
10 <151> PRIOR FILING DATE: 1999-09-14  
12 <150> PRIOR APPLICATION NUMBER: US 09/635,872  
13 <151> PRIOR FILING DATE: 2000-08-10  
15 <160> NUMBER OF SEQ ID NOS: 52  
17 <170> SOFTWARE: PatentIn version 3.1  
19 <210> SEQ ID NO: 1  
20 <211> LENGTH: 928  
21 <212> TYPE: PRT  
22 <213> ORGANISM: Homo sapiens  
24 <400> SEQUENCE: 1

26 Met Leu Phe Lys Leu Leu Gln Arg Gln Thr Tyr Thr Cys Leu Ser His  
27 1 5 10 15  
30 Arg Tyr Gly Leu Tyr Val Cys Phe Leu Gly Val Val Val Thr Ile Val  
31 20 25 30  
34 Ser Ala Phe Gln Phe Gly Glu Val Val Leu Glu Trp Ser Arg Asp Gln  
35 35 40 45  
38 Tyr His Val Leu Phe Asp Ser Tyr Arg Asp Asn Ile Ala Gly Lys Ser  
39 50 55 60  
42 Phe Gln Asn Arg Leu Cys Leu Pro Met Pro Ile Asp Val Val Tyr Thr  
43 65 70 75 80  
46 Trp Val Asn Gly Thr Asp Leu Glu Leu Leu Lys Glu Leu Gln Gln Val  
47 85 90 95  
50 Arg Glu Gln Met Glu Glu Gln Lys Ala Met Arg Glu Ile Leu Gly  
51 100 105 110  
54 Lys Asn Thr Thr Glu Pro Thr Lys Lys Ser Glu Lys Gln Leu Glu Cys  
55 115 120 125  
58 Leu Leu Thr His Cys Ile Lys Val Pro Met Leu Val Leu Asp Pro Ala  
59 130 135 140  
62 Leu Pro Ala Asn Ile Thr Leu Lys Asp Val Pro Ser Leu Tyr. Pro Ser  
63 145 150 155 160  
66 Phe His Ser Ala Ser Asp Ile Phe Asn Val Ala Lys Pro Lys Asn Pro  
67 165 170 175  
70 Ser Thr Asn Val Ser Val Val Phe Asp Ser Thr Lys Asp Val Glu  
71 180 185 190  
74 Asp Ala His Ser Gly Leu Leu Lys Gly Asn Ser Arg Gln Thr Val Trp  
75 195 200 205  
78 Arg Gly Tyr Leu Thr Thr Asp Lys Glu Val Pro Gly Leu Val Leu Met  
79 210 215 220  
82 Gln Asp Leu Ala Phe Leu Ser Gly Phe Pro Pro Thr Phe Lys Glu Thr  
83 225 230 235 240  
86 Asn Gln Leu Lys Thr Lys Leu Pro Glu Asn Leu Ser Ser Lys Val Lys

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87	245	250	255
90	Leu Leu Gln Leu Tyr Ser Glu Ala Ser Val Ala Leu Leu Lys Leu Asn		
91	260	265	270
94	Asn Pro Lys Asp Phe Gln Glu Leu Asn Lys Gln Thr Lys Lys Asn Met		
95	275	280	285
98	Thr Ile Asp Gly Lys Glu Leu Thr Ile Ser Pro Ala Tyr Leu Leu Trp		
99	290	295	300
102	Asp Leu Ser Ala Ile Ser Gln Ser Lys Gln Asp Glu Asp Ile Ser Ala		
103	305	310	315
106	Ser Arg Phe Glu Asp Asn Glu Glu Leu Arg Tyr Ser Leu Arg Ser Ile		
107	325	330	335
110	Glu Arg His Ala Pro Trp Val Arg Asn Ile Phe Ile Val Thr Asn Gly		
111	340	345	350
114	Gln Ile Pro Ser Trp Leu Asn Leu Asp Asn Pro Arg Val Thr Ile Val		
115	355	360	365
118	Thr His Gln Asp Val Phe Arg Asn Leu Ser His Leu Pro Thr Phe Ser		
119	370	375	380
122	Ser Pro Ala Ile Glu Ser His Ile His Arg Ile Glu Gly Leu Ser Gln		
123	385	390	395
126	Lys Phe Ile Tyr Leu Asn Asp Asp Val Met Phe Gly Lys Asp Val Trp		
127	405	410	415
130	Pro Asp Asp Phe Tyr Ser His Ser Lys Gly Gln Lys Val Tyr Leu Thr		
131	420	425	430
134	Trp Pro Val Pro Asn Cys Ala Glu Gly Cys Pro Gly Ser Trp Ile Lys		
135	435	440	445
138	Asp Gly Tyr Cys Asp Lys Ala Cys Asn Asn Ser Ala Cys Asp Trp Asp		
139	450	455	460
142	Gly Gly Asp Cys Ser Gly Asn Ser Gly Gly Ser Arg Tyr Ile Ala Gly		
143	465	470	475
146	Gly Gly Gly Thr Gly Ser Ile Gly Val Gly His Pro Trp Gln Phe Gly		
147	485	490	495
150	Gly Gly Ile Asn Ser Val Ser Tyr Cys Asn Gln Gly Cys Ala Asn Ser		
151	500	505	510
154	Trp Leu Ala Asp Lys Phe Cys Asp Gln Ala Cys Asn Val Leu Ser Cys		
155	515	520	525
158	Gly Phe Asp Ala Gly Asp Cys Gly Gln Asp His Phe His Glu Leu Tyr		
159	530	535	540
162	Lys Val Ile Leu Leu Pro Asn Gln Thr His Tyr Ile Ile Pro Lys Gly		
163	545	550	555
166	Glu Cys Leu Pro Tyr Phe Ser Phe Ala Glu Val Ala Lys Arg Gly Val		
167	565	570	575
170	Glu Gly Ala Tyr Ser Asp Asn Pro Ile Ile Arg His Ala Ser Ile Ala		
171	580	585	590
174	Asn Lys Trp Lys Thr Ile His Leu Ile Met His Ser Gly Met Asn Ala		
175	595	600	605
178	Thr Thr Ile His Phe Asn Leu Thr Phe Gln Asn Thr Asn Asp Glu Glu		
179	610	615	620
182	Phe Lys Met Gln Ile Thr Val Glu Val Asp Thr Arg Glu Gly Pro Lys		
183	625	630	635
			640

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Input Set : A:\210119US0CONT.txt  
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186 Leu Asn Ser Thr Ala Gln Lys Gly Tyr Glu Asn Leu Val Ser Pro Ile  
187 645 650 655  
190 Thr Leu Leu Pro Glu Ala Glu Ile Leu Phe Glu Asp Ile Pro Lys Glu  
191 660 665 670  
194 Lys Arg Phe Pro Lys Phe Lys Arg His Asp Val Asn Ser Thr Arg Arg  
195 675 680 685  
198 Ala Gln Glu Glu Val Lys Ile Pro Leu Val Asn Ile Ser Leu Leu Pro  
199 690 695 700  
202 Lys Asp Ala Gln Leu Ser Leu Asn Thr Leu Asp Leu Gln Leu Glu His  
203 705 710 715 720  
206 Gly Asp Ile Thr Leu Lys Gly Tyr Asn Leu Ser Lys Ser Ala Leu Leu  
207 725 730 735  
210 Arg Ser Phe Leu Met Asn Ser Gln His Ala Lys Ile Lys Asn Gln Ala  
211 740 745 750  
214 Ile Ile Thr Asp Glu Thr Asn Asp Ser Leu Val Ala Pro Gln Glu Lys  
215 755 760 765  
218 Gln Val His Lys Ser Ile Leu Pro Asn Ser Leu Gly Val Ser Glu Arg  
219 770 775 780  
222 Leu Gln Arg Leu Thr Phe Pro Ala Val Ser Val Lys Val Asn Gly His  
223 785 790 795 800  
226 Asp Gln Gly Gln Asn Pro Pro Leu Asp Leu Glu Thr Thr Ala Arg Phe  
227 805 810 815  
230 Arg Val Glu Thr His Thr Gln Lys Thr Ile Gly Gly Asn Val Thr Lys  
231 820 825 830  
234 Glu Lys Pro Pro Ser Leu Ile Val Pro Leu Glu Ser Gln Met Thr Lys  
235 835 840 845  
238 Glu Lys Lys Ile Thr Gly Lys Glu Lys Glu Asn Ser Arg Met Glu Glu  
239 850 855 860  
242 Asn Ala Glu Asn His Ile Gly Val Thr Glu Val Leu Leu Gly Arg Lys  
243 865 870 875 880  
246 Leu Gln His Tyr Thr Asp Ser Tyr Leu Gly Phe Leu Pro Trp Glu Lys  
247 885 890 895  
250 Lys Lys Tyr Phe Gln Asp Leu Leu Asp Glu Glu Ser Leu Lys Thr  
251 900 905 910  
254 Gln Leu Ala Tyr Phe Thr Asp Ser Lys Asn Thr Gly Arg Gln Leu Lys  
255 915 920 925  
258 <210> SEQ ID NO: 2  
259 <211> LENGTH: 328  
260 <212> TYPE: PRT  
261 <213> ORGANISM: Homo sapiens  
263 <400> SEQUENCE: 2  
265 Asp Thr Phe Ala Asp Ser Leu Arg Tyr Val Asn Lys Ile Leu Asn Ser  
266 1 5 10 15  
269 Lys Phe Gly Phe Thr Ser Arg Lys Val Pro Ala His Met Pro His Met  
270 20 25 30  
273 Ile Asp Arg Ile Val Met Gln Glu Leu Gln Asp Met Phe Pro Glu Glu  
274 35 40 45  
277 Phe Asp Lys Thr Ser Phe His Lys Val Arg His Ser Glu Asp Met Gln  
278 50 55 60

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TIME: 13:19:44

Input Set : A:\210119US0CONT.txt  
Output Set: N:\CRF3\07232001\I895072.raw

281 Phe Ala Phe Ser Tyr Phe Tyr Tyr Leu Met Ser Ala Val Gln Pro Leu  
282 65 70 75 80  
285 Asn Ile Ser Gln Val Phe Asp Glu Val Asp Thr Asp Gln Ser Gly Val  
286 85 90 95  
289 Leu Ser Asp Arg Glu Ile Arg Thr Leu Ala Thr Arg Ile His Glu Leu  
290 100 105 110  
293 Pro Leu Ser Leu Gln Asp Leu Thr Gly Leu Glu His Met Leu Ile Asn  
294 115 120 125  
297 Cys Ser Lys Met Leu Pro Ala Asp Ile Thr Gln Leu Asn Asn Ile Pro  
298 130 135 140  
301 Pro Thr Gln Glu Ser Tyr Tyr Asp Pro Asn Leu Pro Pro Val Thr Lys  
302 145 150 155 160  
305 Ser Leu Val Thr Asn Cys Lys Pro Val Thr Asp Lys Ile His Lys Ala  
306 165 170 175  
309 Tyr Lys Asp Lys Asn Lys Tyr Arg Phe Glu Ile Met Gly Glu Glu  
310 180 185 190  
313 Ile Ala Phe Lys Met Ile Arg Thr Asn Val Ser His Val Val Gly Gln  
314 195 200 205  
317 Leu Asp Asp Ile Arg Lys Asn Pro Arg Lys Phe Val Cys Leu Asn Asp  
318 210 215 220  
321 Asn Ile Asp His Asn His Lys Asp Ala Gln Thr Val Lys Ala Val Leu  
322 225 230 235 240  
325 Arg Asp Phe Tyr Glu Ser Met Phe Pro Ile Pro Ser Gln Phe Glu Leu  
326 245 250 255  
329 Pro Arg Glu Tyr Arg Asn Arg Phe Leu His Met His Glu Leu Gln Glu  
330 260 265 270  
333 Trp Arg Ala Tyr Arg Asp Lys Leu Lys Phe Trp Thr His Cys Val Leu  
334 275 280 285  
337 Ala Thr Leu Ile Met Phe Thr Ile Phe Ser Phe Phe Ala Glu Gln Leu  
338 290 295 300  
341 Ile Ala Leu Lys Arg Lys Ile Phe Pro Arg Arg Arg Ile His Lys Glu  
342 305 310 315 320  
345 Ala Ser Pro Asn Arg Ile Arg Val  
346 325  
349 <210> SEQ ID NO: 3  
350 <211> LENGTH: 305  
351 <212> TYPE: PRT  
352 <213> ORGANISM: Homo sapiens  
354 <220> FEATURE:  
355 <221> NAME/KEY: SIGNAL  
356 <222> LOCATION: (1)..(24)  
357 <223> OTHER INFORMATION:  
360 <400> SEQUENCE: 3  
362 Met Ala Ala Gly Leu Ala Arg Leu Leu Leu Leu Gly Leu Ser Ala  
363 1 5 10 15  
366 Gly Gly Pro Ala Pro Ala Gly Ala Ala Lys Met Lys Val Val Glu Glu  
367 20 25 30  
370 Pro Asn Ala Phe Gly Val Asn Asn Pro Phe Leu Pro Gln Ala Ser Arg  
371 35 40 45

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PATENT APPLICATION: US/09/895,072

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TIME: 13:19:44

Input Set : A:\210119US0CONT.txt  
Output Set: N:\CRF3\07232001\I895072.raw

374 Leu Gln Ala Lys Arg Asp Pro Ser Pro Val Ser Gly Pro Val His Leu  
 375 50 55 60  
 378 Phe Arg Leu Ser Gly Lys Cys Phe Ser Leu Val Glu Ser Thr Tyr Lys  
 379 65 70 75 80  
 382 Tyr Glu Phe Cys Pro Phe His Asn Val Thr Gln His Glu Gln Thr Phe  
 383 85 90 95  
 386 Arg Trp Asn Ala Tyr Ser Gly Ile Leu Gly Ile Trp His Glu Trp Glu  
 387 100 105 110  
 390 Ile Ala Asn Asn Thr Phe Thr Gly Met Trp Met Arg Asp Gly Asp Ala  
 391 115 120 125  
 394 Cys Arg Ser Arg Ser Arg Gln Ser Lys Val Glu Leu Ala Cys Gly Lys  
 395 130 135 140  
 398 Ser Asn Arg Leu Ala His Val Ser Glu Pro Ser Thr Cys Val Tyr Ala  
 399 145 150 155 160  
 402 Leu Thr Phe Glu Thr Pro Leu Val Cys His Pro His Ala Leu Leu Val  
 403 165 170 175  
 406 Tyr Pro Thr Leu Pro Glu Ala Leu Gln Arg Gln Trp Asp Gln Val Glu  
 407 180 185 190  
 410 Gln Asp Leu Ala Asp Glu Leu Ile Thr Pro Gln Gly His Glu Lys Leu  
 411 195 200 205  
 414 Leu Arg Thr Leu Phe Glu Asp Ala Gly Tyr Leu Lys Thr Pro Glu Glu  
 415 210 215 220  
 418 Asn Glu Pro Thr Gln Leu Glu Gly Gly Pro Asp Ser Leu Gly Phe Glu  
 419 225 230 235 240  
 422 Thr Leu Glu Asn Cys Arg Lys Ala His Lys Glu Leu Ser Lys Glu Ile  
 423 245 250 255  
 426 Lys Arg Leu Lys Gly Leu Leu Thr Gln His Gly Ile Pro Tyr Thr Arg  
 427 260 265 270  
 430 Pro Thr Glu Thr Ser Asn Leu Glu His Leu Gly His Glu Thr Pro Arg  
 431 275 280 285  
 434 Ala Lys Ser Pro Glu Gln Leu Arg Gly Asp Pro Gly Leu Arg Gly Ser  
 435 290 295 300  
 438 Leu  
 439 305  
 442 <210> SEQ ID NO: 4  
 443 <211> LENGTH: 5597  
 444 <212> TYPE: DNA  
 445 <213> ORGANISM: Homo sapiens  
 447 <400> SEQUENCE: 4  
 448 cggagccgag cggcggtccg tcgccggagc tgcaatgagc ggcccccga ggctgtgacc 60  
 450 tgcgcgcggc ggcccgaccg gggccccctga atggcggctc gctgaggcgg cggcgccgc 120  
 452 ggcggctcaag ctcctcggg gcgtggcggt gcgggtgaagg ggttatgttgc ttcaagctcc 180  
 454 tgcagagaca aacctataacc tgcctgtccc acaggtatgg gctctacgtg tgcttcttg 240  
 456 gcgtcggttgc caccatcgtc tccgccttcc agttcggaga ggtggttctg gaatggagcc 300  
 458 gagatcaata ccatgttttgc ttgtattcc atagagacaa tattgttgc aagtcccttc 360  
 460 agaatcggttgc ttgtctgccc atgcccatttgc acgttgttta cacctgggttgc aatggcacag 420  
 462 atcttgaact actgaaggaa ctacagcagg tcagagaaca gatggaggag gagcagaaaag 480  
 464 caatgagaga aatccttggg aaaaacaccaa cggAACCTAC taagaagagt gagaagcagt 540  
 466 tagagtgtttt gctaacacac tgcattaagg tgccaatgct tgtactggac ccagccctgc 600

Use of n and / or Xaa has been detected in the  
 Sequence Listing. Review the Sequence Listing  
 to ensure a corresponding explanation is present  
 in the <220> to <223> fields of each sequence  
 using n or Xaa.  
*KYJ*

VERIFICATION SUMMARY  
PATENT APPLICATION: US/09/895,072

DATE: 07/23/2001  
TIME: 13:19:45

Input Set : A:\210119US0CONT.txt  
Output Set: N:\CRF3\07232001\I895072.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application No  
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:1120 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10  
L:2207 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17  
L:2211 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17  
L:2213 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17  
L:2754 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23  
L:2926 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35